GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

\*

protein - protein search, using sw model ĕ

March 14, 2001, 16:12:15; Search time 14.09 Seconds (without alignments) 578.602 Million cell updates/sec Run on:

US-09-455-486-6 2351 Title: Perfect score: Sequence:

1 MESISMMGSPKSLSETCLPN.....ALVLPSIVILDLLQLCRYPD 454

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

174772 segs, 17957048 residues Searched:

174772 Total number of hits satisfying chosen parameters:

Mir Max

DB seq length: 0 DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*
.: /cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
.: /cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*
.: /cgn2\_6/ptodata/2/laa/6\_COMB.pep:\*
.: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
.: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
.: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
.: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
.: /cgn2\_6/ptodata/2/laa/Packfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appli	Appli	Appli	Appli	App11	Appli	Appli	Appli	Appli	Appli	Appli	Appli	App1i	Appli	Appli	Appli	Appli	Appli	App11	Appli	Appli	Appli						
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ı		-521	7-886-2	-855	-974A	-57	1-974A	- 99	-30	1-983-2	1-97	8	-53	9-9	1-54	1-84	9-09	5-11	3-00	-83	2-87	1-53	2-90	3-54	50-1	3-18	1-39	-097	-54
		-083	-487	-482	-724	3	1-724-	-841-997A	08-290-301-	08-588	US-08-588	08-651-999A-	¥	-476	4	-484-840-2	3-483-094-2	-805	-348-	-800-	-022-875-2	-404-531B-6	-476-900A-6	-488-546A-6	-121-057	-509-187D	-121-396-4	PCT-US93-09704A-4	-580-545B-2
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US-09-262-653A-2 US-08-724-394A-9 US-08-968-463-14 US-08-473-553A-3 US-08-473-553A-5 US-08-473-553A-6 US-08-473-553A-2 US-08-473-553A-2 US-08-473-553A-2 US-08-916-902A-3 US-08-916-902A-3 US-08-916-902A-3 US-09-213-389-3 US-09-759-568-2 US-08-930-996A-8 US-08-930-996A-8 US-08-930-996A-10 US-08-930-996A-10
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882 882 82.5 82.5 80 80 80 80 79 79 79 79 79
330 330 331 331 332 333 344 444 5444 5444

## ALIGNMENTS

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General information: |DZ(e)| = OS|EL|V General information: |DZ(e)| = OS|EL|V General information: Lal, preeti APPLICANT: Lal, preeti APPLICANT: Gotley, Wail C. TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: STREET: 3174 PORTER DRIVE
                                        1026 = 05/22/48
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,521
FILING DATE: Herewith
                Sequence 1, Application US/09083521 Patent No. 6048970
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                          CITY: PALO ALTO STATE: CALIFORNIA
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; CLONE: 1691243
US-09-083-521-1
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US-09-083-521-1
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ö 0; Gaps Length 141; Indels Query Match 31.3%; Score 736; DB 3; I Best Local Similarity 100.0%; Pred. No. 5.9e-70; Matches 141; Conservative 0; Mismatches 0;

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314 MVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL 373

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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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                                                      374 LAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFV 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dimeric glycoprotein receptor extracellular domains, hydrophilic
1 MVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: putative amino-terminal extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM MS-DOS Version 4.0
SOFTWARE: VAX/YMS MASS11 VIA REFMIT to IBM MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  APPLICANT: Kelton, Christie Ann
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vul Yen
APPLICANT: Nugent, No. 5744448een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein IDENTIFICATION METHOD: domains, hydrophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity to other G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: putative transmembrane region I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                          Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane domain
                                                                                                                                                                                                                                                Sequence 2, Application US/08487886
Patent No. 574448
                                                                                                                                121 LALVLPSIVILDLLQLCRYPD 141
                                                                                                            434 LALVLPSIVILDLLQLCRYPD 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
INPERATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: signal sequence LOCATION: -17 to -1
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 RSTYNLKKLP----TLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILRQE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-----LLSFFFAMVHVA-----YSLCLPMRRSERYLFLNMAYQQVHANIEN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.6%; Score 107.5; DB 1; Length 695;
Best Local Similarity 17.0%; Pred. No. 0.011;
Matches 84; Conservative 77; Mismatches 148; Indels 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 putative carboxy-terminal intracellular
                                                   protein-coupled receptor hydrophobic, about 20-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity to other G
protein-coupled receptor
hydrophobic, about 20-23
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                         similarity to other G
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IDENTIFICATION METHOD: .'-''
                                                                                                                                                                                                                                                                  NAME/KEY: putative transmembrane region III
                                                                                                                                                                                                                                                                                                                                                                                                                    putative transmembrane region IV
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                                                                                                                          putative transmembrane region II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: putative transmembrane region v LOCATION: 512 to 533
IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled rec-
IDENTIFICATION METHOD: hydrophobic, about
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                                                 to 404
METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
to 370
METHOD:
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614 to 678
                    IDENTIFICATION IDENTIFICATION
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IDENTIFICATION
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